



010898 03/11/03

#14

010898  
SEQUENCE LISTING

&lt;110&gt; Nippon Zeon Co., Ltd.,

&lt;120&gt; Modified DNA molecules, Recombinants and uses thereof

&lt;130&gt; J209

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 4

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1306

&lt;212&gt; DNA

<213> *Mycoplasma gallisepticum*

&lt;220&gt;

&lt;223&gt; TTM-1 gene

&lt;400&gt; 1

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ataaaatata	cttaatattc	tatgaataag	aaaagaatca	tcttaaagac	tattagttt	240
tttaggtacaa	catccttct	tagatttggg	atttctagct	gtatgtctat	tactaaaaaa	300
gatgcaaacc	caaataatgg	ccaaacccaa	ttagaagcag	cgcgaatgg	gttaacagat	360
ctaatcaatg	ctaaagcgat	gacattagct	tcaactacaag	actatgcca	gattgaagct	420
agtttatcat	ctgcttatag	tgaagctgaa	acagtttata	ataacctta	tgcaacat	480
gaacaactaa	aatggctaa	aactaattta	gaatcagcc	tcaaccaag	taatcggat	540
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actttagaac	aacgtgctac	taaccttggaa	ggtttgcatt	caactgctt	taatcaaatt	660
cgcaataatt	tagtggatct	atacaataaa	gctagtagtt	taataactaa	aacactagat	720
ccactaaatg	ggggAACGCT	tttagattct	aatgagat	ctacagtta	tcggaatatt	780
aataatacg	tatcaactat	taatgaacaa	aagactaatg	ctgtgcatt	atctaataatg	840
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tataaaatatg	caagaaggac	cgttggaaat	ggtgatgaa	cttcaagtag	aattcttgc	1020
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taccaattt	gttttagcaa	ctatggtcca	tcaactgg	atttatattt	cccttataag	1140
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gttcaacaag	ttgagtttgc	cacttcaact	agtgcacaa	atactacagc	taatccaact	1260
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&lt;210&gt; 2

&lt;211&gt; 3189

&lt;212&gt; DNA

<213> *Mycoplasma gallisepticum*

&lt;220&gt;

&lt;223&gt; mgc3 gene

&lt;400&gt; 2

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010898

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gttcatttaa	aaAGAAATTAA	taCTAACTCA	aATAGAAATTG	gtaATAGAAA	caACAATTCT	480
aagttgtaa	ttGGTGGTGT	tgATAATCCA	gCTCACGTA	ttAGATTAC	TGATGATGGG	540
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tCTTTCAAT	tagATGAAA	atTTGTTTAT	ccAGAAATGGA	CTGGTCTGA	AGAGAAATAAA	960
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gAGTACTTA	ttCAAAATGG	gtTCACTAGT	caAGTGGTA	gAAACTCTGT	tACAAACCAA	2580
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gCTGTTAG	gtGCTGGTA	atCTGGTAT	aaGAAACCTG	ctGCTGCTGC	taAAACCTGCT	3060
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<213> *Mycoplasma gallisepticum*

&lt;220&gt;

&lt;223&gt; TTM-1 portion of pNZ40K-S

&lt;400&gt; 3

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Page 2

010898

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 20               25               30  
 val val Ser Ser Val Gln Leu Ser Glu Glu Glu Ser Thr Phe Tyr Leu  
 35               40               45  
 Cys Pro Pro Pro Val Gly Ser Thr Val Ile Arg Leu Glu Phe Gly Cys  
 50               55               60  
 Met Ser Ile Thr Lys Lys Asp Ala Asn Pro Asn Asn Gly Gln Thr Gln  
 65               70               75               80  
 Leu Glu Ala Ala Arg Met Glu Leu Thr Asp Leu Ile Asn Ala Lys Ala  
 85               90               95  
 Met Thr Leu Ala Ser Leu Gln Asp Tyr Ala Lys Ile Glu Ala Ser Leu  
 100              105              110  
 Ser Ser Ala Tyr Ser Glu Ala Glu Thr Val Asn Asn Leu Asn Ala  
 115              120              125  
 Thr Leu Glu Gln Leu Lys Met Ala Lys Thr Asn Leu Glu Ser Ala Ile  
 130              135              140  
 Asn Gln Ala Asn Thr Asp Lys Thr Thr Phe Asp Asn Glu His Pro Asn  
 145              150              155              160  
 Leu Val Glu Ala Tyr Lys Ala Leu Lys Thr Thr Leu Glu Gln Arg Ala  
 165              170              175  
 Thr Asn Leu Glu Gly Leu Ser Ser Thr Ala Tyr Asn Gln Ile Arg Asn  
 180              185              190  
 Asn Leu Val Asp Leu Tyr Asn Lys Ala Ser Ser Leu Ile Thr Lys Thr  
 195              200              205  
 Leu Asp Pro Leu Asn Gly Gly Thr Leu Leu Asp Ser Asn Glu Ile Thr  
 210              215              220  
 Thr Val Asn Arg Asn Ile Asn Asn Thr Leu Ser Thr Ile Asn Glu Gln  
 225              230              235              240  
 Lys Thr Asn Ala Asp Ala Leu Ser Asn Ser Phe Ile Lys Lys Val Ile  
 245              250              255  
 Gln Asn Asn Glu Gln Ser Phe Val Gly Thr Phe Thr Asn Ala Asn Val  
 260              265              270  
 Gln Pro Ser Asn Tyr Ser Phe Val Ala Phe Ser Ala Asp Val Thr Pro  
 275              280              285  
 Val Asn Tyr Lys Tyr Ala Arg Arg Thr Val Trp Asn Gly Asp Glu Pro  
 290              295              300  
 Ser Ser Arg Ile Leu Ala Asn Thr Asn Ser Ile Thr Asp Val Ser Trp  
 305              310              315              320  
 Ile Tyr Ser Leu Ala Gly Thr Asn Thr Lys Tyr Gln Phe Ser Phe Ser  
 325              330              335  
 Asn Tyr Gly Pro Ser Thr Gly Tyr Leu Tyr Phe Pro Tyr Lys Leu Val  
 340              345              350  
 Lys Ala Ala Asp Ala Asn Asn Val Gly Leu Gln Tyr Lys Leu Asn Asn  
 355              360              365  
 Gly Asn Val Gln Gln Val Glu Phe Ala Thr Ser Thr Ser Ala Asn Asn  
 370              375              380  
 Thr Thr Ala Asn Pro Thr Pro Ala Val Asp Glu Ile Lys Val Ala Lys  
 385              390              395              400  
 Ile Val Leu Ser Gly Leu Arg Phe Gly Gln Asn Thr Ile Glu Leu Ser  
 405              410              415  
 Val Pro Thr Gly Glu Gly Asn Met Asn Lys Val Ala Pro Met Ile Gly  
 420              425              430  
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 <213> Mycoplasma gallisepticum

010898

<223> MGC3 encoded by mgc3 gene

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50 55 60  
Phe Asn Thr Val Leu Arg Asp Val Asp Asn Phe Ile Thr Ala Ala  
65 70 75 80  
Asn Gly Thr Ile Ile Lys Leu Asp Ser Phe Thr Lys Pro Leu Tyr Gly  
85 90 95  
Leu Asp Leu Ser Asp Asp Cys Gly Gly Tyr Lys Val Lys Gln Ile Val  
100 105 110  
Ser Asp Tyr Thr Ser Arg Asn Arg Phe Asp Gln Arg Gln Thr Arg  
115 120 125  
Ala Tyr Tyr Ala Leu Leu Val Asn Asp Glu Ala Asn Val His Leu Lys  
130 135 140  
Arg Ile Asn Thr Asn Ser Asn Arg Ile Gly Asn Arg Asn Asn Asn Ser  
145 150 155 160  
Lys Phe Val Ile Gly Gly Val Asp Asn Pro Ala His Val Ile Arg Phe  
165 170 175  
Thr Asp Asp Gly Thr Lys Phe Asn Phe Thr Asn Gln Thr Gln Gly Glu  
180 185 190  
Ile Val Asn Asp Phe Ile Leu Asp Ala Pro Ile Leu Pro Lys Asp Leu  
195 200 205  
His Pro Asp Trp Tyr Asn Leu Tyr Ile Gln Arg Lys Ile Leu Pro Asn  
210 215 220  
Asp Val Asn Thr Ala Val Val Pro Trp Pro Val Gly Arg Val Ser Gly  
225 230 235 240  
Thr Asn Ala Asp Asp Gly Met Phe Asp Cys Gly Asn Gln Ile Thr  
245 250 255  
Asn Thr Asp Pro Ile Ala Gln Thr Lys Thr Thr Asp Asn Gln Asn  
260 265 270  
Pro Ser Thr Phe Asn Ser Gly Ala Met Pro Gly Ala Asn Asn Arg Tyr  
275 280 285  
Asp Ser Gln Leu Asn Val Lys His Arg Ile Lys Thr Ser Phe Gln Leu  
290 295 300  
Asp Glu Arg Ile Asn Thr Asn Ser Asn Arg Ile Gly Asn Arg Asn Asn  
305 310 315 320  
Asn Ser Lys Phe Val Ile Gly Gly Val Asp Asn Pro Ala His Val Ile  
325 330 335  
Arg Phe Thr Asp Asp Gly Thr Lys Phe Asn Phe Thr Asn Gln Thr Gln  
340 345 350  
Gly Glu Ile Val Asn Asp Phe Ile Leu Asp Ala Pro Ile Leu Pro Lys  
355 360 365  
Asp Leu His Pro Asp Trp Tyr Asn Leu Tyr Ile Gln Arg Lys Ile Leu  
370 375 380  
Pro Asn Asp Val Asn Thr Ala Val Val Pro Trp Pro Val Gly Arg Val  
385 390 395 400  
Ser Gly Thr Asn Ala Asp Asp Gly Met Phe Asp Cys Gly Asn Gln  
405 410 415  
Ile Thr Asn Thr Asp Pro Ile Ala Gln Thr Lys Thr Thr Asp Asn  
420 425 430  
Gln Asn Pro Ser Thr Phe Asn Ser Gly Ala Met Pro Gly Ala Asn Asn  
435 440 445  
Arg Tyr Asp Ser Gln Leu Asn Val Lys His Arg Ile Lys Thr Ser Phe  
450 455 460

010898

Gln Leu Asp Glu Lys Phe Val Tyr Pro Glu Trp Thr Gly Ser Glu Glu  
465 470 475 480  
Asn Lys Asn Ile Thr Arg Leu Ala Thr Gly Ser Leu Pro Ser Asn Glu  
485 490 495  
Arg Tyr Trp Ile Leu Asp Ile Pro Gly Thr Pro Gln Val Thr Leu Lys  
500 505 510  
Glu Asp Ser Val Asn Val Phe Ser Arg Leu Tyr Leu Asn Ser Val Asn  
515 520 525  
Ser Leu Ser Phe Ile Gly Asp Ser Ile Tyr Ile Phe Gly Thr Ser Glu  
530 535 540  
Leu Pro Ser Leu Trp Tyr Ser Phe Pro Thr Arg Leu Ser Asp Leu  
545 550 555 560  
Thr Ala Leu Asn Gln Val Lys Thr Asp Asp Ile Glu Ala Ser Ser Thr  
565 570 575  
Asp Asn Gly Thr Thr Asn Gly Thr Thr Ala Asp Thr Ser  
580 585 590  
Ser Gly Ser Thr Gly Ala Gly Thr Gly Asn Thr Asn Thr Ser Gln  
595 600 605  
Thr Val Ser Asn Pro Thr Leu Asn Thr Tyr Arg Ser Phe Gly Ile Asp  
610 615 620  
Ser Lys Pro Thr Ser Ala Asn Lys Ile Asp Glu Thr Asn Trp Ala Asp  
625 630 635 640  
Pro Asn Val Ile Glu Ala Arg Ile Tyr Ala Glu Tyr Arg Leu Gly Ile  
645 650 655  
Gln Asn Glu Ile Pro Ile Thr Asn Ala Gly Asn Phe Ile Arg Asn Thr  
660 665 670  
Ile Gly Gly Val Gly Phe Thr Ser Thr Gly Ser Arg Val Val Leu Arg  
675 680 685  
Ala Ser Tyr Asn Gly Asp Gln Arg Pro Thr Gly Asn Phe Gln Pro Phe  
690 695 700  
Leu Tyr Val Phe Gly Tyr Leu Gly Tyr Gln Gln Thr Arg Thr Gly Thr  
705 710 715 720  
Phe Trp Tyr Gly Thr Tyr Lys Leu Leu Asn Asn Ser Pro Tyr Asp Val  
725 730 735  
Leu Asp Ser Pro Arg Val Gly Thr Glu Thr Asn Gln Phe Arg Arg Thr  
740 745 750  
Ser Leu Thr Tyr Pro Val Met Gly Gly Tyr Leu Thr Glu Glu Gly Ala  
755 760 765  
Arg Ser Phe Ser Asn Thr Pro Tyr Ile Arg Ala Gln Gly Asp Thr Pro  
770 775 780  
Glu Ser Arg Ser Ile Phe Gln Ser Gly Tyr Ser Asp Asn Thr Tyr Glu  
785 790 795 800  
Tyr Ile Gln Ser Val Leu Gly Phe Asp Gly Ile Arg Asn Asn Leu Asn  
805 810 815  
Val Gly Val Lys Ala Ser Ser Phe Leu Asn Ser Asn Arg Pro Asn Pro  
820 825 830  
Asn Gly Leu Glu Met Ile Ala Ala Thr Thr Tyr Leu Arg Ser Gln Ile  
835 840 845  
Gly Leu Ala Arg Thr Ser Gly Leu Pro Asn Gln Gln Pro Phe Gly Thr  
850 855 860  
Thr His Gln Val Ile Ser Val Ser Pro Gly Asp Gln Phe Ser Ser Ile  
865 870 875 880  
Lys Asn Ile Arg Thr Ile Phe Pro Gly Asn Gln Leu Trp Tyr Phe Leu  
885 890 895  
Phe Thr Asn Glu Asn Asn Lys Ser Ser Val Tyr Thr Leu Arg Leu Ala  
900 905 910  
Asp Ser Ser Asn Pro Asp Ala Ser Ser Ser Phe Ser Pro Thr Ser Leu  
915 920 925  
Ile Asp Val Asn Glu Ile Gly Val Ile Leu Pro Leu Leu Asp Asn Ser  
930 935 940  
Phe Tyr Thr Val Asn Ala Ala Gly Asn Val Ala Leu Phe Ser Ser Asn  
945 950 955 960  
Pro Gly Ser Pro Gly Ser Tyr Thr Ala Val Asn Thr Phe Asn Gln Asn

010898

965 970 975  
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980 985 990  
Phe Trp Gly Thr Ile Gln Phe Lys Pro Asp Glu Tyr Leu Ile Gln Asn  
995 1000 1005  
Gly Phe Thr Ser Gln Val Ala Arg Asn Phe Val Thr Asn Gln Ser Phe  
1010 1015 1020  
Leu Asn Ser Leu Val Asp Phe Thr Pro Ala Asn Ala Gly Thr Asn Tyr  
1025 1030 1035 1040  
Arg Val Val Val Asp Pro Asp Gly Asn Leu Thr Asn Gln Asn Leu Pro  
1045 1050 1055  
Leu Lys Val Gln Ile Gln Tyr Leu Asp Gly Lys Tyr Tyr Asp Ala Lys  
1060 1065 1070  
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1075 1080 1085  
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1105 1110 1115 1120  
Ala Gln Arg Lys Leu Gln Asp Lys Gly Phe Lys Thr Thr Phe Lys Lys  
1125 1130 1135  
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Thr Gln Thr Ala Asn Val Lys Lys Pro Ala Ala Leu Gly Ala Gly  
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Pro Lys Ser Gly Ala Pro Thr Lys Pro Thr Ala Pro Lys Pro Ala Ala  
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